

Gencore version 5.1.4-p5-4578									
Copyright (c) 1993 - 2003 Compugen Ltd.									Sequence 159, APP
OM nucleic - nucleic search, using sw model									
Run on: April 15, 2003, 03:00:20 ; Search time 310.707 Seconds									
(without alignments) 4571.527 Million cell updates/sec									
Title: US-09-001-737-7									
Perfect score: 1661									
Sequence: 1 GAATTCGGCTCATATGGCA.....TGGCGCGATAAGCGGAATC 1661									
Scoring table: IDENTITY_NUC									
Gappen 10.0 , Gapext 1.0									
Searched: 593429 seqs, 438583590 residues									
Total number of hits satisfying chosen parameters: 1186858									
Minimum DB seq length: 0									
Maximum DB seq length: 200000000									
Post-processing: Minimum Match 0%									
Maximum Match 100%									
Listing first 45 summaries									
Database :									
Published_Applications_NA: *									
1: /cgn2.6/ptodata/1/publicra/US07_PUBCOMB.seq: *									
2: /cgn2.6/ptodata/1/publicra/US06_NEWM_PUB.seq: *									
3: /cgn2.6/ptodata/1/publicra/US06_PUBCOMB.seq: *									
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10: /cgn2.6/ptodata/1/publicra/US09_PUBCOMB.seq: *									
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12: /cgn2.6/ptodata/1/publicra/US10_PUBCOMB.seq: *									
13: /cgn2.6/ptodata/1/publicra/US60_NEWM_PUB.seq: *									
14: /cgn2.6/ptodata/1/publicra/US60_PUBCOMB.seq: *									
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.									
SUMMARIES									
Result No. Score Query Length DB ID Description									
1 1038.4 62.5 1926 9 US-10-267-311-50 Sequence 50, Appl									
2 942.6 56.7 3625 10 US-10-267-311-50 Sequence 42, Appl									
3 615.8 37.1 640681 10 US-09-700-988-1 Sequence 1, Appl									
4 589.8 215.5 10 US-09-950-488-13 Sequence 5, Appl									
5 530.4 31.9 1635 10 US-09-801-122-360 Sequence 13, Appl									
6 483.6 27.9 1617 9 US-08-738-982A-266 Sequence 380, APP									
7 464.2 27.8 1617 9 US-10-267-311-20 Sequence 266, APP									
8 461.6 27.7 1617 9 US-10-267-311-28 Sequence 20, APP									
9 460 27.6 1623 9 US-09-122-363-23 Sequence 20, APP									
10 458.6 27.6 1623 9 US-10-267-311-3 Sequence 23, APP									
11 458.6 27.6 1620 9 US-10-267-311-16 Sequence 16, APP									
12 458.6 27.6 3309400 9 US-09-738-626-5 Sequence 1, APP									
13 458.4 27.6 3309400 9 US-10-069-059-7 Sequence 7, APP									
14 457.2 27.5 2130 9 US-09-738-626-296 Sequence 2986, APP									
15 457 27.5 1644 9 US-10-069-059-5 Sequence 5, APP									
16 456.4 27.5 2241 9 US-10-069-059-11 Sequence 11, APP									
17 456.2 27.5 2175 9 US-10-069-059-11 Sequence 9, APP									
18 455.6 27.4 2073 9 US-10-069-059-9 Sequence 19, APP									
19 453.4 27.3 1735 12 US-10-069-059-19 Sequence 19, APP									
RESULT 1									
US-10-267-311-50									
SEQUENCE 1									
US-10-267-311-50 Application US10267311									
GENERAL INFORMATION									
APPLICANT: Siegel, Marvin									
APPLICANT: Chu, N. Randall									
APPLICANT: Mizzen, Lee A.									
TITLE OF INVENTION: INDUCTION OF THI-LIKE RESPONSE IN VITRO									
FILE REFERENCE: 12071/02001									
CURRENT APPLICATION NUMBER: US10/267,311									
CURRENT FILING DATE: 2002-10-09									
PRIORITY APPLICATION NUMBER: US09/613,303									
PRIORITY FILING DATE: 1999-07-08									
NUMBER OF SEQ ID NOS: 55									
SOFTWARE: FASTSEQ for Windows Version 4.0									
SEQ ID NO 50									
LENGTH: 1926									
TYPE: DNA									
ORGANISM: Artificial Sequence									
FEATURE: OTHER INFORMATION: fusion sequence									
FEATURE: NAME/KEY: CDS									
LOCATION: (1)...(1923)									
Query Match Score 62.5%; Length 1926; DB 9; Best Local Similarity 77.3%; Pred. No. 2.26-24; Matches 1258; Conservative 0; Mismatches 366; Indels 0; Gaps 0;									
Sequence 1, Appl									
Sequence 2, Appl									
Sequence 3, Appl									
Sequence 4, Appl									
Sequence 5, Appl									
Sequence 6, APP									
Sequence 7, APP									
Sequence 8, APP									
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Sequence 11, APP									
Sequence 12, APP									
Sequence 13, APP									
Sequence 14, APP									
Sequence 15, APP									
Sequence 16, APP									
Sequence 17, APP									
Sequence 18, APP									
Sequence 19, APP									
Sequence 20, APP									
Sequence 21, APP									

LENGTH: 3625 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 42:
 ; US-09-070-927A-42

Query Match 55.7%; Score 942.6; DB 10; Length 3625;
 Best Local Similarity 74.2%; Pred. No. 8.9e-221; O; Mismatches 415; Indels 0; Gaps 0;

Qy 15 ATGCGAAAGAACTAACATTTCAGCAGTGGCGCGCGCCATGGCGGAGGTAT 74
 Db 364 ATGGCAGAAAGAGNNTTAAAGTTCAGAAGATGGACGAGTACGCTACCGAGT 423

Qy 75 ATGTTAACGAGTACCGCAAGTAACGCTGGTCTTAAGGSGCGCATGTTGCTTGAA 134
 Db 424 GTTACCGAGTACAGTACGCTAGCATTAGCCCTTAAAGGTTGAGCTTAAAGGTTGAA 483

Qy 135 AAAGCTTCTGTTCCCTTAATCTATGCGGGTACACATTCTAAAGGATGCAA 194
 Db 484 AAATCACTTCTGGTACCTATGATCTACAGTACGATGGTAACTCTGAGGAATGAA 543

Qy 195 TTAGAGATCATTTGAAACATGGGACAAATAGTGTCTGACTGCTTGTAAACC 254
 Db 544 TTGGAGATCATTTGAAACATGGCCAAATATGTTGAGAAGTGTCTTAAACG 603

Qy 255 ATGATATCTCTGTATGGACGACTACTSCAACGTTGACAGCCATGTTCAT 314
 Db 604 ATGATATCTCTGGTGAAGGACACAAACGCGACGTTTACACAAAGCCATTGTCGT 663

Qy 315 GAGGAGCTAAATGAGCAGCAGGCTATCCAAATGGCATCGTGGACCGATGAA 374
 Db 664 GAGGCTTAAACAGTGTGACGCTGGTACGCAACCCATTGGATGGTGGATGAA 733

Qy 375 ACAGCACACACAGGTGAAAGCAGCTGCAACCTGTATGGCAAG 434
 Db 724 TTAGCAGAAACAGGAGTGGAGATACATATTCATCTCTGATGTTGAA 783

Qy 435 GAGCTATCTCTGGTGGCGTGTGGCAACCTGTGGTAA 494
 Db 784 GAGGCTGTGACAGTGTGGCGTGTGGCTTCACAGTTCTGAAAGTGGCAATTA 843

Qy 495 TCGAGCTTGGGGCTGTGGCAACCTGTGGTAA 554
 Db 844 GCGGAGCAATGGGAAAGTGGTAAAGGCCGCTTAATCCATGAGAACTAAAGG 903

Qy 555 ATGGAACAGAATGTGAGTGTGAGGCTGCAATTGACCGTGTAACTGTCTCAA 614
 Db 904 ATTGAAACAGAAATTAGTGTGTTGAGGAATGCAATTGACCGCGGTATATCTCAA 963

Qy 615 TACATGTCAGACAGCATGAAATGTCAGCTGGTAAACCCATTCTTAATC 674
 Db 964 TACATGTCAGACAGCATGAAATGTCAGCTGGTAAACCCATTCTTAATC 1023

Qy 675 ACGGAAACAAACTGTCACACATCAGACTGCAAGACTTGTGCAACTTGAGTCATAA 734
 Db 1024 ACGGAAACAAACTGTCACACATCAGACTGCAAGACTTGTGCAACTTGAGTCACA 1083

Qy 795 GCTGAAATAGATGTTGTTGACTCTGCACTGGTGTGCAACAGGCCAGGTTGT 854
 Db 1144 GATTGAAATCCTGTTGACTTAATGTCAGTAAAGGCGCCAGATGG 1203

Qy 855 GATCCGCGGAGACTATGCTGAGATATTCTGAGCTGGAGGCTGACGTGATTA 914
 Db 1204 GACCGCCGCAAGCGGATGCTGAGATATTCTGAGCTGGAGTACACTA 1263

Qy 915 GAGGAGCTGGACTTAAAGGAGTGTGACAACTGAGCCCTGGAGGCTGCTAAG 974

Db 1264 GACGACTTAGGGTTAGTAAAGACACACTTGTAAACTTGGAAATCTTGCAA 1323
 Qy 975 ATTACAGTGTGATAAGATAACAGATGTTGAACTGGTGGAGGTTCAGAGCTAT 1034
 Db 1324 GTAGTGTGCGACAGATACACACAAATGTCGAAGAGCTGCTGCTAAAGGCTT 1383

Qy 1035 GCTACCGTATTGCGACTGTTAAATCCAAATGAAACAGAACACTCTGACTTGCCT 1094
 Db 1384 GATGCCGGTCTCATTTAAACAAATCGGAAACAGCTGCTGATTGATGGT 1443

Qy 1095 GAAACTACAGAAGTGGAAATTAGCTGGTGTGAGCTTACAGTAACTGAA 1154
 Db 1444 GAAATTCAGAAGCTTGTAGTAAATTAGCTGGTGGTGGTAAAGTCGT 1503

Qy 1155 GTCACAGAGACGCTTAAAGAAATGACCTGTTGAGGTTGCTAAAGCT 1214
 Db 1504 GCTGACATGAAACAAATTAAGGAAATTAGTAAAGGTTGAGATGCTTAAACCA 1563

Qy 1215 ACACATGCGCGTGTGAAAGAGTATGTTGCGTGTGGTGGAGACACTTATAGGT 1274
 Db 1564 ACCTGCGCGTGTGAAAGAGGCGATGGTCTGTTGTTGCTGCGACTGTTAATGTA 1623

Qy 1275 ATGAAAGATGACCTCTGTGACTGTTGAGGGCATATGCTACTGGCGTAACTTG 1334
 Db 1624 ATGTTAAAGTGTGCTGGTGTAGGAGTTGAGGGATGTTGCAACAGGATCAAGTGC 1683

Qy 1335 CTTGGTCTGAGAGCTGTGACTGCTCAATTGCTTAATGTGGTGTGAGGCTTC 1394
 Db 1684 GTCCTGCATTGAGAAACAACTCCAAATGCGAAATGCTGTTTATGAGGATCA 1743

Qy 1395 GAACTATGACAAATGTTGAAACACGCCGAGGACAGATTATGCTCCACAGT 1454
 Db 1744 GTGATGTTGAGAACTTAAAGATGTGACTTGTGTTGAGTTCGSGATGTCAGTCACGGT 1803

Qy 1455 GAGGGGTGATTTAAACAGGAACTATGACCTGACCTGTCAGAAATGACGATCG 1514
 Db 1804 GATGGAAACATGTTTGTGACATGTTTAAAGGAAATGCTGTTTAAACAGTACGTC 1863

Qy 1515 CTTCAAATGACGTCTGTTGACTCTATTTGCAACAGAGAGCTGTTGCTAAT 1574
 Db 1864 TTCAAAATGCACTCTGTGAGTTTATTAACACTGAGGCTGTTGAGCAG 1923

Qy 1575 AACCTGACCGCTTGCCTGAGGCAAGCATCCACAGTGG 1620
 Db 1924 AACCGAGACCCTGCAACAGCTCCATTGATGATGTCATCATG 1969

RESULT 3
 ; US-09-070-988-1
 ; Sequence 1, Application US/09790988
 ; Patent No. US2012767A1
 ; GENERAL INFORMATION
 ; APPLICANT: SHIGENBU, SHUJI
 ; APPLICANT: WATANABE, HIDEMI
 ; APPLICANT: HAYTORI, MASANIRA
 ; APPLICANT: SAKAI, YOSHIOUKI
 ; TITLE OF INVENTION: GENOME DNA OF BACTERIAL Symbiont OF APHIDS
 ; FILE REFERENCE: 081350/0139
 ; CURRENT APPLICATION NUMBER: US/09790,988
 ; CURRENT FILING DATE: 2001-02-23
 ; PRIOR APPLICATION NUMBER: JP2000-107160
 ; PRIOR FILING DATE: 2000-04-07
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 60681
 ; TYPE: DNA
 ; ORGANISM: Buchnera sp.
 ;
 Query Match 37.1%; Score 615.8; DB 10; Length 640681;
 Best Local Similarity 65.8%; Pred. No. 1.5e-139; O; Mismatches 582; Indels 6; Gaps 2;
 ; US-09-070-988-1
 ;

QY 18 GCAAAAGAAATCAATTTCAGCGAGATGCCGTCGCTCCATGGCGGGAGTTGATG 77
 Db 18721 GCTAAAGATGTAAATTTGGAAATGAGCCGATTAATGCTTCGTGAGTTAATG 18780
 QY 78 TTACAGAGATACCTCCTAAGCTAACCTTACCGCTTGCCPAANGGGCAATGTGTG 137
 Db 18731 TTACAGAGATCGTAAAGTGTACTTAAAGCCATAGGAACTAAGTGAATG 18840
 QY 138 GCTTTCGGTCTCCCTTTACTAATGAGGGTACCTTGTAAAGAGATGCGATTA 197
 Db 18841 TCTTTCGGACCCCTGGTACTTAACTTAAAGATGGGTATCCCTAGCCGTAA 18900
 QY 198 GAGATCATTGAAACATGGGAGAAATTGGTGTGAGTGGTAAACCAT 257
 Db 18901 GAGAGATAATTCGAAACATGGGAGCTCAAGTGAATGAACTTGATCAA 18960
 QY 258 GATATGCTGGATGGGAGACTACTGACACGCTTGTGACGAAAGCCTGTGCAA 317
 Db 18961 GATGCAGCAGGGATGGTACCAACACAGGAACTTAAACCAT 19020
 QY 318 GAGCTAAAAATGTCAGCAGCAGTGGCTAACTGGCTCAAGTGAATGAA 377
 Db 19021 GGTGTAAGGCTGAGCTGACACTCTGTTGATGAACTGAACTGAAATG 19080
 QY 378 GCAACAGCAACGCTGTTGAAAGGCACTGCTCAACCTTATGCAACAT 437
 Db 19081 GCTGTTACGCTGCTGTTGAAAGGCAATTTCTGTTACATGAACTG 19140
 QY 438 OCTATTGCTCAGTCGCTCAGTCTACATCAGCCTC --TGAAAACTGGAGATATC 494
 Db 19141 GCAAACTACAGTGTGACTATTTCTGCAATTCGAGATGAAACTGTT 19200
 QY 495 TCAGAGCTATGGCTGTTGGCAACGATGGTATTACACTCAGAACTCGGGT 554
 Db 19201 CGAGAGCAATGGAAAGTGTGTTATGAGGTTATGAGGATGAGCTGGT 19260
 QY 555 ATGGAACAGACTGAAAGTGTGTTATGAGGATGCAATTGACGGTGTACCTGTC 614
 Db 19261 TTACAGGATGACTGTTGACAGGTCAGGATTTGATCGTGTATCTCC 19320
 QY 615 TACATGGTCAGACGAACTGAAATGGCTGAGGCTCTGAAACCCATTCTAC 674
 Db 19321 TATTATTCATTAACCGAGAACGATTTGTTGATTGAGAAACCATATATG 19380
 QY 675 AGGGTAAAGATGTCACACCTTCAAGCTTCAAGCTTCCAGACATTTGCCCTACTTGTGAA 734
 Db 19381 GCTGCTAAAAATATCTAATGTTGTGAAATGTTACCAATTTCAGTGTG 1940
 QY 735 ACCACCGTCATTACATGATTCAGATGTTGAGCTGACACCTTCACCTT 794
 Db 19441 TCAGGAAACCACTTATTATTTCTGAGATTAGGGTGAACCTTACCAATT 19500
 QY 795 GCTCTGACACAGATCGGGTACITCAATGGGTGCTGAACGCCGAGATTGGT 854
 Db 19501 GTACTTAACTCATGAGGATTAAAGCGAGCTAAAGACCTGATGGT 19560
 QY 855 GATCGTGTAAAGCTCTGAGACATGCTACTTCAGCAGGGTACAGGATACA 914
 Db 19561 GATCGTGTAAAGCACTTCAAGATTTCAATCTGTTGTTGTATCT 19620
 QY 915 GAGGATCTGAGCTGTTAAAGATGCTCAAGACGCTGCCCTGGACAGCTG 974
 Db 19621 GAGGATAGTGTGTTGAGTAACTTACTTAAAGGTTAGGAAACAGT 19680
 QY 975 ATTACAGTGTAAAGTGTGAGCTGTTGAGGTTCTGGAGGTGCAAGATTT 1034
 Db 19681 GTGTTTAACTGAAAGCACTACACTTATTTGGTGTGTTGAGGAAACCTC 1094
 QY 1035 GCTACCGTATGGCTGACTTAATCGCAATTAGGAAACACACTCTACTTGACCGT 1094
 Db 19741 CAAGTCGTATTAACTCAACCGAGAAATCAAGAGCTCTCTGATGATAA 19800

QY 1095 GAAAACTTCAAGACCTTGGGAAATTGCTGTTGCTGTTGAGTCAACTTGA 1154
 Db 19801 GAAATAATTAATGAACTGCTTAACTTCAAGGGGTGTCGAGTAAAGTGT 19860
 QY 1155 GCTCCACAGAGAGCTTAAGAGAAATGAACTTCTGGCATGTTAGATCT 1214
 Db 19861 GGGCTTACAGACTAATGAAAGAAAACCTGTTGAGTGAATGCT 19920
 QY 1215 ACACCCGCGCTGAGAGGTTGCTGCTGTTGAGCTACATTACGGT 1274
 Db 19921 ACTCGTGCACTGTAGAGGAGGTGTTCTGAGGTGTTGCTGATG 19980
 QY 1275 ATTGAAAGTAGCAGCTTGAGCTGAGGGCATGATGTTACGGGTT -- ACAT 1331
 Db 19981 GCAAGGAAATAGCTTACGGTGTCAATGAGTCAGCAGGTTGAGGT 20040
 QY 1332 GRCGTCGCTCTAGAGGCTGAGCTGCAATGTTAATGCTGGGACRC 1391
 Db 20041 GCTTGTGCGTGTGAGGTTCTGAGTGTGAACTGAACTGAACT 20100
 QY 1392 GCGGTTAGTACAGTGAAGAAAGGCTCAGGAGGTTCTGAGGTTCTGAGACCT 1451
 Db 20101 TCTGTTGTTACACATTTAAAGAGGGAACTGTTCTGAGTCACTGAGCT 20160
 QY 1452 GCTGAGTGGTGTATGTTAAACGGATCTGCTGTCAGTACAGGTTCT 1511
 Db 20161 GATGAGTATGAGTGTGAGTGTGAGTTGAGTATGACCAACTAAGTTCAGGTCT 20220
 QY 1512 GCGCTTAAATGAGCTCTGTGAGCTGTTATTGACAAAGAGCTGTTCT 1571
 Db 20221 GCTTGTACATATCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCT 20280
 QY 1572 AATAAACCTGAGGACCTA 1590
 Db 20281 GACTTGCCAAAGGAGATA 20299

RESULT 4
 US-09-960-428-13
 ; Sequence 13, Application US/09960428
 ; Patent No. US20020115147A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Roche Diagnostics GmbH
 ; TITLE OF INVENTION: Method for producing an active heterodimeric AMV-RT in prokary
 ; FILE REFERENCE: 5272/00
 ; CURRENT APPLICATION NUMBER: US/09/960,428
 ; CURRENT FILING DATE: 2001-09-21
 ; NUMBER OF SEQ ID NOS: 22
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 13
 ; LENGTH: 2155
 ; TYPE: DNA
 ; ORGANISM: Escherichia coli
 ; US-09-960-428-13

Query Match: 35 %; Score 589.8; DB 10; Length 2155;
 Best Local Similarity 61.3%; Pred. No. 1.7e-34;
 Matches 986; Conservative 0; Mismatches 617; Indels 6; Gaps 2;

QY 18 GCAAAAGAAATCAATTTCAGCAGATGGGGCGCCATGGCCGGGAGTTGATG 77
 Db 478 GCTAAAGAGCTTAACTTCTGGTAACTGAGCTGCTGGTAACTA 537
 QY 78 TTACAGAGTACGGTAAAGTAACTGCTTAAAGGGCGCAATGTTGTTGAA 137
 Db 538 CTGGCAGTGGCTAAAGTACCCCTGGCTCAAAGGCCGTAACGTTGCTGATAA 597
 QY 138 GCTTTCGGTCTCCCTTAATCTACTTATGAGGGTACCTCTGCTAATG 197
 Db 598 TCTTGTGCGACGCCATCACCACAGGTTGCTGTTGCTGAACTG 657
 QY 198 GAGATCATTGAAACCTGGGAAATTGGTGTCTGAGGGTCTTAACCAAT 257

Db 658 GAAGACAAGTTCGAAATAATGGTGGCCAGATGGTGAAGAAGTTCCTTAAGCAAC 717
 Qy 258 GATATTGCTGGTATGGACGGGAGCTACTGCAACAGTTTGACAAAGCATTTGTCATGA 317
 Db 718 GACCTTGAGGGGGTACACCACTGCAACCGTACTGCTCAGGTTACACAGCGAA 777
 Qy 318 GGACTAAATAATGTCACAGCAGGGTCTAATCCATTGGTTCTCGTCAAGGATGAA 377
 Db 778 GGTCAGAAGCTGTTGGCGGCTAGTGAACCGATGGCTGAAACOTGTTGACAAA 837
 Qy 378 GCAACAGCAACAGCTGGTGAAGGCTTGCAAGAACGATTCGTCACCTGATGCAAGAA 437
 Db 838 GCGGTTACCGCTGCACTGAGAAGCTGAGTCAGTGAAGGGCTGTCGTTACCATCTAA 897
 Qy 438 GCTTATGTCAGTGGCTGCACTGAGTCACTCCCT--TGAAGAAAGTGGAGTATC 494
 Db 898 GCGATGCTCGAGGTGTTGACATCTCCGTTACTCGGACGACACCGTAGTAACGTC 957
 Qy 495 TCAAGAACGACTGAGTGAAGTGGTGAAGGCACTGCAATTCGAGAATTCGAGGT 554
 Db 958 GCTGAAAGCAGTGGACAAAGTGGTAAAGACGCTTACCTGAGACGCTGAGACGTACCGT 1017
 Qy 555 ATGCAACAGACTGAGTGAAGTGGTGAAGGCACTGCAATTCGAGAATTCGAGGT 614
 Db 1018 CTACGAGGACGAGCTGAGCTGGTGAAGTGGTGAAGGCACTGCAATTCGAGGT 1077
 Qy 615 TACATGTCAGAGCAATGAAATAATGGTGGAGCTTGACGTTGAGCTGGTGCACCGTCCT 674
 Db 1078 TACTCTCATCACAGCCGAGACTGGCTGAGTAGCTGAGACCGCTTCACCGCT 1137
 Qy 675 ACGGATAAAAGTCAACATCAACGATTCGAGCTTGCCACTACTGAGACTCTAA 734
 Db 1138 GCTCACAGAATACTCCACATCGCGAATGCTCCGTTGAGCTGTCGCAA 1197
 Qy 735 ACCAACCGTCATCATCATCATATGCAATGATGAGGGAGAACACTTCACCTT 794
 Db 1198 GCGAGCAACCGCGTGTGATCATGCTGAAAGTGGAGGGAGCGCTGGGACTCTG 1257
 Qy 795 GCTCTGACAAAGTCTGGTACTTCATGCTGGTGAAGGCACTTGCACTGAGCTTAA 854
 Db 1258 GTCTGTCACCATGCTGCGTGTGAGTAAAGCACCGCCGCTGGC 1317
 Qy 855 GATCCGCGTAAGCTATGCTGAGCACATTGCTATCTGAGCTGGTGTACGGTACCA 914
 Db 1318 GATGTCGTTAAAGTGTGTCAGATTCGACATTCGAAACCGTGACTGGCTGACGGTCT 1377
 Qy 915 GAGGAGCTGAGCTGTGATTAAGATGCTCAATGACGCCCTGAGACGGCTGTAAG 974
 Db 1378 GAGAGATCTGTTGAGCTGAGCTGAAAGCAACCGTGGCTGAGACTGGCTAACGT 1437
 Qy 975 ATTCAGTGTATAAGATGACAGCTGTTGGGGTCTGGAGGTCAAGAGCTTAA 1034
 Db 1438 GTCTGTCACACAGACACCACTATCGTGGGGTGGTGAAGAAGCTGGCAATC 1497
 Qy 1035 GCTAACCGTATGCACTGATTAATGCAATAGAACACACTCTGACTTGACCGT 1094
 Db 1498 CAGGGCGCTGCTGCTGAGCTGGCTGAGGTTGAGAAGCAGCTGACTGGACCGT 1557
 Qy 1095 GAAACTACAGACCTTGGCGAAATGCTGGTGTGCTGTTACAGATAGGA 1154
 Db 1558 GAAAGCTGAGGACCGCTGAGCTGACACTGCGAGCGCTGAGCTTACAGRGGT 1617
 Qy 1155 GCTCCACAGAGCACCTTAAGAAATGAACTGCACTGCAATGAGCTTAATGCT 1214
 Db 1618 GCTGCTACAGTGAATGAGAAAGCACCGTGGAGATGCCGACCG 1677
 Qy 1215 ACACGTCGACCGCTGAGGAGGATGTTGCTGCTGTTGAGACGACTTATAGGT 1274
 Db 1678 ACCCGTGTGCGGTAGAGAGGGGGTGTCTGGTGGGGTGTGGCTGATCCCGTA 1737
 Qy 1275 ATGAAAGATGAGCTGAGCTGAGCTGGCGCTGAGGTTGCTGACTGGAGTACA 1331
 Db 1738 GCGCTTAAGTGTGAGCTGAGCTGGCTGAGGAGGACGACCTGGGTATCAGAT 1797

RESULT 5
 Sequence 380 Application US/09841132
 Patent No. US20030061848A1
 GENERAL INFORMATION:
 APPLICANT: Bhatia, Ajay
 APPLICANT: Skeky, Yair A. W.
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
 DIAGNOSIS OF CHLAMYDIAL INFECTION
 FILE REFERENCE: 21012.463C8
 CURRENT APPLICATION NUMBER: US09/09841,132
 NUMBER OF SEQ ID NOS: 599
 SOFTWARE: FASTSEQ For Windows Version 3.0/4.0
 SEQ ID NO: 380
 LENGTH: 1635
 TYPE: DNA
 ORGANISM: Chlamydia pneumoniae
 US-09-09841-132-580

Query Match: 31.9%; Score: 530.4; DB: 10; Length: 1635;
 Best Local Similarity: 59.5%; Pred. No.: 5.2e-120;
 Matches: 957; Conservative: 0; Mismatches: 636; Indels: 15; Gaps: 3;

Qy 18 GCAAGAAAGATTAATTTTCAGAGCTGGCTGGCTCCATGGCGGGAGTATG 77
 Db 7 GCGAAATAATTAATATATGAGGAGCCAGAAAAAAATACTAAGGGTAACCT 66
 Qy 78 TTAGGAGATACCGTAACTAACGCTGGCCCTAAAGGGCCAAATGTTGTTCTGAA 137
 Db 67 CTGCGAGAGCTAAAGTACTCTGGCCPAAGGAGTCACCTGTTATGATG 126
 Qy 138 GCTTGTGTCCTTAATCTGAGGGTAACCATGCTAAAGATGGATTA 197
 Db 127 AGCTTGCTCCCAACTGCTAAAGTGGTTCTGTTACGAAATGAGCTC 186
 Qy 198 GAAATCTTGTGAAACATGGAGGAAATGTTGCTGAAATGGCTCTAACACAT 257
 Db 187 GAGCAACATGAAACATGGGGCTGAGCTGAAAGTCGCCCCGAAACTCTG 246
 Qy 258 GATATTGTTGAGGGAGCTACTGACAGTTGACAAAGCCATGTCAGAA 317
 Db 247 GACAAAGGGAGGAGGAACTACAGACGACTGTTCTGAGGAACTATAGGA 306
 Qy 318 GGACTAAATAATGTCACAGCAGTGGTAAATCCTGTTACCGTGTGCTGAGGAA 377
 Db 307 GGTCTAAGATGTCACGGCTGCGTGCACATCCPCTGACCTAAAGAGGTACGAGAA 366
 Qy 378 GCAACAGCTGTTGAGGCTGAAAGCCATGCTGAACTGTTCTGCAAGGAA 437

Db 367 GCCCTAAAGTGTGTGATGACTAAAAAATTAGTAACCTGACACATACAAA 426
 Qy 438 CTTATGCTCGCGCTGAGTCATCACCTCTGA --AAAGTTGGAGGTATC 494
 Db 427 GAAATCCTCAGTAGTACTATCTCAGCAATAATGATTCGAAATCTGTT 486
 Qy 495 TCGAAGCTATGAGCGCTGGCAGATGCGACATGATGCAACATCTCAGGT 554
 Db 487 GCGAAAGCTGGAGAAAGTGTGTTAACACGATCATTGTTGAGAGCTAAGGC 546
 Qy 555 ATGAAACACAACTGAGGTGGTGAAGCGCATTTGACCGTGTGTTACCGTCA 614
 Db 547 TCGAAACTGTCGACGGTGTAGGAACTGACCTCACCGTGATACCTCGAC 606
 Qy 615 TACATGTCAGACGAACTGAGAAATGGTGCAGGCCTGAAACCCATTACTATC 674
 Db 607 TACTTCGCCACAACTCCAGAAACTCAGAATGCGTTTGAAGACCCCTGATC 666
 Qy 675 ACGATAAAAGTGTAAACATCCAGAACTTGGACTACTTGAGGAGTCTAA 734
 Db 667 TAGATTAACAAACTCTGGATTAAGTAACTGAGCTTCAAGCCAGATTTG 726
 Qy 735 ACCAACCGTCATACATCATTCAGATGATGGATGGTGAACACTCCACCT 794
 Db 727 TCGGACGCCCTCTTATCATGTCAGAAGAACTGAGGAACTGAGCTTACACTA 786
 Qy 795 GTTTGGACAGAATCTGGACTTCATGGTCTGTCAGGGCAGGATTTG 854
 Db 787 GTATGTCATGAGTCGCCAGGAGTCAGCTGAGTCAGTCAGTCCTGTT 846
 Qy 855 GATCGCTGTAANSTAGTCGTTGAGACATGCTACTGACAGGGTACAGTAA 914
 Db 847 GAGAGAAGAAGAAAGTGTGAGACCTCGTACATCTACTGGGCCACTAGT 906
 Qy 915 GAGGATCTAGGCTGATTAAGATGAGCTCAAGACAGCCTGAGCAGCTG 974
 Db 907 GAGAAACTGCGTGAACATGAGAACTGAGCTTACACTGAGCTTACAGA 966
 Qy 975 ATTACAGTCGTTAGATGAGCTGAGCTGATTTACTGTGTGAGGTCTGG 1034
 Db 967 GTTACCTACTAAAGAAGATACACATCTCGAGCTTGGAAACATGATC 1026
 Qy 1035 GCTAACCGTATTCACTGATTAATCCAACTAGAACACACTCGACTTGACCT 1094
 Db 1027 CAAGCTGATGCCAAATATTAAACAAACAAATCGAGATAGCAGTACAGAA 1086
 Qy 1095 GAAAAACTCAAAACACCTTGGCAAAATTACTGTGTGAGCTATCAAACTGA 1154
 Db 1087 GAAACTCCAAAGCTTGCACACTCTCCGGTGTGCCGATTCGGTGG 1146
 Qy 1155 GCTCACACAGAGCAGCTTAAGAAATGAACTTCACATGAGCTTAATGGT 1214
 Db 1147 GCTGCTACGGAAATGAGTAAGAGAAAGACAGACTGAGTGTGACACGCA 1206
 Qy 1215 ACATGCGACCCCTGAGAGGATGTTGCTGTGAGCAGCACTTATGGT 1274
 Db 1207 ACATGCGACCTGAGGAACTCCTCCCTGGTGGACTGCTTGTGG 1266
 Qy 1275 ATGAAACTGCGCTCTGAGCTGAGGAACTCCTCCCTGGTGGACTGCTTGTG 1325
 Db 1267 ATCCCTACACTAAAGCTTCTCTCTGATGAGAACAGGAGCTTGGT 1326
 Qy 1326 AACATGTCGCTCGTCTGATGAGACCCCTGAGCTTAATGCTTAATCTGGTAC 1385
 Db 1327 CGTATATCTAAAGCTTACGCTCAATTAGCAAGTACCGCAGTAA 1386
 Qy 1385 GAGGGCTGGTACTTATGAGCTGAAACAGCGCTGAGGAGACGGATTATCT 1445
 Db 1387 GAAAGGCTCTTCAGCACTCTACGAACTGAGCTGAAATGANGCTATG 1446
 Qy 1446 GACACGGTGTGGGTGTGATGATGATAACAGGAACTGACCTGACCGCTG 1505
 Db 1447 TACAGTGCTTATACAGATATGTTGAGGAGTATTAGTCACATGACT 1506
 Qy 1506 CGATCAGGCGCTCAAAATCAGCTGTTGAGCTAGTCTTATTGACACAGGACTT 1565
 Qy 1507 CGCTCAGCTCTAGAGACGCCAGCTTACGAGGTTACTCTCAGAACAGGCCTA 1566
 Qy 1566 GTGCTATAAACCTGAA --CCGCTACCCAGGCCAGGATGCCA 1610
 Db 1567 ATCGCTGATACCCAGAGAACTCTCTCAGTCAGGATGCCA 1614

RESULT 6
 US-08-781-986A-266
 ; Sequence 266, Application US/08781986A
 ; Publication No. US2003054436A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Charles Kunsch
 ; TITLE OF INVENTION: *Staphylococcus aureus* Polynucleotides and Sequences
 ; NUMBER OF SEQUENCES: 5255
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Human Genome Sciences, Inc.
 ; STREET: 9410 Key West Avenue
 ; CITY: Rockville
 ; STATE: Maryland
 ; COUNTRY: USA
 ; ZIP: 20850
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
 COMPUTER: HP Vectra 486/33
 OPERATING SYSTEM: MS-DOS version 6.2
 SOFTWARE: ASCII Text
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/781,986A
 FILING DATE:
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 REGISTRATION NUMBER: 30,446
 PRIORITY DOCUMENT NUMBER: P2248PP
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (301) 309-8504
 TELEFAX: (301) 309-8512
 INFORMATION FOR SEQ ID NO: 266:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1017 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 ; US-08-781-986A-266
 Query/Match 29.1%; Score 493.6; DB 7; length 1017;
 Best Local Similarity 67.2%; Pred. No. 1.2e-10;
 Matches 681; Conservative 2; Mismatches 331; Indels 0; gaps 0;
 Db 308 TGTTCATGAGCTAAATGAGCAACCGAGTGTCTCATCATGTTATCCGAGG 367
 Qy 1 TTTCAGAGGCTTGGAAATGTTGAGCTGTTACGAGG 60
 Db 368 CATGAAACGACAGACAGACAGCGTTGAGCTCTGAAAGCCATTGCTAACCTGATC 427
 Qy 61 TATCGACAAACGAGCTTAATGTTGAGCTGTTACGAAATCTCAAAAGTGA 120
 Qy 428 TGGCAAGAGCTTGTCTAGGCTGCTGAGCTATCATACGCTGAAAGATGAGA 487
 Db 121 AAATTAACAAATGCGCAAGTGGCAAGTGGCTGAGGAGATGAGATGGAGC 180
 Qy 488 GATATCTCAGAACTATGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 547
 Db 181 TATATCTCAGACTGAAAGTAGTACGTTGCTACATGATGATGATGATGATC 240
 Qy 548 TCGGGTATGGAACAGACAGTGAAGTGTGAGGAGTCAATTGACCGTGTGTTACCT 607

ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: fusion sequence
 NAME/KEY: CDS
 LOCATION: (1)..(2844)
 US-10-267-311-20

Query Match 27.8%; Score 461.6; DB 9; Length 2847;
 Best Local Similarity 55.9%; Pred. No. 4.9e103; Gaps 0;
 Matches 878; Conservative 0; Mismatches 694; Indels 0; Gaps 0;

Db 841 GACCCACGCAAGGGTTCATGGTGTCTGGCTTCATGTCACCAAGGAACTGGCTCGAT 900
 Qy 915 GAGGATCTGGGCTTGTGAAATTAAAGATGTCATCATGACAGCCCTTGACAGCGCTAG 974
 Db 901 CCAGAGTGGCTAACCTCAACGAGCTAACGAGCTGGGGTTCGAGCTACCGACCGCGC 960
 Qy 975 ATTACACTGTGAAAGATGAGTACGAGCTGAGTGTGAGGTTGAGAGTCAAGTACAGT 1034
 Db 961 ATCACCGGTTCCAGACGACAAACCATCGTGTGAGTGTGAGCTGGTCCGGAGAAGCT 1020
 Qy 1035 GCTAACCCATATGCACTGACTGTTAAATGCAATPTGAAACACAACTCTGACTTGACCGT 1094
 Db 1021 GAGGACCGCTGGGGCAGTCGTCGGCAAGTCCACGACCATGCGTGGCATGGTCCGGAGCT 1080
 Qy 1095 GAAACTACAGAAGCTGGAAATTAGCTGGTGTGACTGTTTGTGAGTCAAGTGGGA 1154
 Db 1081 GAAAGGAGAAGAGCGTTGCTGATCTCCGGTGGTATGCTGTCATCCGGTGGT 1140
 Qy 1155 GCTCCAGAGAGACGCTTAAAGAAATGAAACACTTGATGTTAGATGATGTCAATGCT 1214
 Db 1141 GCGCAACTGAAACCGAGTCACGACCCAAAGCTGGCTGCAACCCATGCGTGGCATAC 1200
 Qy 1215 ACAGTGAGCCGAGCACAGACGCTTACGCTGGTGGTGGAGAACACACTTATACCGTT 1274
 Db 1201 GCTGGCCGAGCACAGACGCTTACGCTGGTGGTGGTGGTGGTGGTGGTGGTGGCATAC 1260
 Qy 1275 ATGCA-----AAAGTAGSCGCTTGTGAGCTGGGGATATCTGAGCTAC 1328
 Db 1261 GCTGAGACTCTGAAAGCTTACGCCAGAGTGTGAGGAGCTGGGGTTCGG 1320
 Qy 1329 ATTCGGCTCTGGCTCTGAGAAGCTGACCTCAATGCTTAAATGCTGGTGGAA 1388
 Db 1321 GCACTGCTGACTGCTGTTGGAGCAGGGTACTTGATGCCCTCCACCGGGCTTGAC 1380
 Qy 1389 GGCTCGTAGTTATGACAGTTGAAACACGCCCTGGAGAACACAGATTATGCGCA 1448
 Db 1381 GGCTCTGGTGTGAGCTGAGCTGCTCTCGCAAGGGAGGCTCACGGTCA 1440
 Qy 1449 ACAGGTGAGGGTGTGATGATTAACAGGAACTATGACCCCTCAAGTACAGA 1508
 Db 1441 ACTTTGAGATGGAACTGATCACAGCAGGTTGATGACCCAGTCAGGTACCCAT 1500
 Qy 1509 TCAGCGCTTCAATGAGCTGCTGTTGAGCTTATTTGACACAGAGGTGT 1568
 Db 1501 TCCCGAGTAGTGAATGACCTCTTGGCACGATGTTGACCTGAGCTGGCTCGTT 1560
 Qy 1569 GCTTAAACCTGACCG 1587
 Db 1561 GTTGAGAGCTGCAGG 1579

RESULT 8
 US-10-267-311-20
 ; Sequence 20, Application US/10267311
 ; Publication No. US20030050469A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Siegel, Marvin
 ; APPLICANT: Chu, N. Randolph
 ; APPLICANT: Madsen, L.A.
 ; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
 ; FILE REFERENCE: 12017/002001
 ; CURRENT APPLICATION NUMBER: US/10/267,311
 ; CURRENT FILING DATE: 2002-10-19
 ; PRIORITY FILING DATE: 2000-07-10
 ; PRIORITY APPLICATION NUMBER: US/00/613,303
 ; PRIORITY FILING DATE: 1999-07-15
 ; NUMBER OF SEQ ID NOS: 55
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ ID NO: 20
 ; LENGTH: 2847
 ; TYPE: DNA

Query Match 27.8%; Score 461.6; DB 9; Length 2847;
 Best Local Similarity 55.9%; Pred. No. 4.9e103; Gaps 0;
 Matches 878; Conservative 0; Mismatches 694; Indels 0; Gaps 0;

Db 58 CATAAGCCAGACATTTGGTACGAGGAAAGGGCTCCGGGCTTGAGGGGCTG 117
 Qy 72 GATATGTTGAGACATGCCAACAGTAACTGTTGCTCTAAGGGCAATTTGTTCT 1311
 Db 118 AACGCCCTGGCGATGGPAAMGGTACCTTGGCCCAAGGGCCGAACCTCCCTG 177
 Qy 132 GAAACGCTTGGTCTCTTAATGACGAGCTGTTGGCTGAAATGGGAACTTGA 191
 Db 178 GAAAGAATGGGGTCCCAAGGACATGGGGTCAATGGGAACTTGAAGGATC 237
 Qy 192 GAAATGAGATCATTTGAAACATGGGCAATATGGCTGTAATGGCTCTAA 251
 Db 238 GGCTGGAGATCGTACGGAGATGGGGCAAGCTGGCCAGCTGAAAGTACGAG 297
 Qy 252 ACCATGATATGCTGTCATGGGACGACTCTGCAACAGTTGACACAAGCCATGTT 311
 Db 258 ACCGATGAGTGGCGGTGCGCAGCACCCACGGGACCCGGCACGGTGTGGCCAGGGTGGT 357
 Qy 312 CATGAGGACTAAATGAGCAGCAGGGTCTATCATTGTTGTTGAGTCTGGAGGATT 371
 Db 358 CGCGGGGCGCTGGCACCTCGGGGGGACCCGGCAGCCGGCGCGTCAGGGCAGTC 417
 Qy 372 GAAACGACACGACACACTGTTGAGGCTTGAAGGATTCACCTGCTACCTGTTCTGC 431
 Db 418 GAAAGGCGTGTGAGGAGGAGGACCTCGACGGCGCAAGGAGCTGGCAGGAC 477
 Qy 432 AAGGAGTATGCTGAGTCGTCGTCGTTGAGTCACTCATCGCTGCTGAAAGTGGAGCAT 491
 Db 478 AAGGGCCAGATGCGGCCACCGCAGGGATTCGGGGGTGACCTGGTACCTG 537
 Qy 492 ATCTAGAGCTATGGAGGTTGGGCAAGGAGGTTGTTGATACATCGAGAACTGGA 551
 Db 538 ATGGCGGGCGATGACAGGGGGCAACGGGGCTCTACCGTGGAGGAGTCCAC 597
 Qy 552 GGTATGGAACGAACTTGTGAGGCTGACCTGGTGAACCTGAAACCTTATCTTA 611
 Db 598 ACCCTTGCGTCGACCTCGTGGAGGCTGACGGGGTACGGGGTGTGACAGGGTACCTCG 657
 Qy 672 ATCACGGTTAAAGTGCACACCTCCAGACGATTTGCACTACTTGAGGAGTTCT 731
 Db 718 CTGGTCACTCCAAAGTGGCTACGTCAGGAGCTGCTGCGCTGAGGTCTC 777
 Qy 732 AAACACCCGTCATCTCATTTGAGGAGTGTGATGAGCTGAGCTTCACCC 791
 Db 778 GGAGCCGCTAACCGCTGGTGAATCATCGGGAGGCTGCGGGAGGGCTGTCACC 837
 Qy 792 CTGGCTGAGAGATGTTGAGCTTGTGTTGTTGTTGCTCTCAAGGCCAGATT 851
 Db 838 CTGGCCCTCACAGATGCGGCACTTCAGTCGTCGGGGTCAGGGCTCCGGCTC 897
 Qy 852 GGTATGCTGTAAGCTATGTTGAGACGATGCTATCTGACAGGTGGTCACTGTT 911
 Db 898 GGCAACCCGCAAGGCTGAGCTGAGGATATGGCCATCTCACCGTGGCTAGTGTAC 957
 Qy 912 ACAGGGCTGAGGACTTAAAGATGCTACATGACGAGCCCTGGACAGCTGGCT 971

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Db 958 AGCGAAGAGGCTGGCTGACCTGGGACCTGGCTGGCAAGGCCGC 1017
Qy 972 AAGATAGTAACTGATATAAGATACAGATATGTTGAAAGGTCTGAACT 1031
Db 1018 AAGGCGCTGGTCACCAAGGACAGACCCATCTGGCGGCGCTGACCGACCC 1077
Qy 1032 ATTGCTAAACGATGATGCACTGATTAATCCGAACTCTGACITTTGAC 1091
Db 1078 ATCGCCGACGAGTGGCCAGATGCCAGAGACAGACTCGGACAGACAG 1137
Qy 1092 CGTGTAAACATACAGAAGGTTGGCGAAATAGCUGCGTGGTGTAGTGTAAAGTA 1151
Db 1138 CGTGTAGAGCTCGCAGGAGGGCTGGCCAAAGCTGGCGGTGGTGTGCGGAGTCAGCC 1197
Qy 1152 GGAGCTCCAACTAGAGACAGCTTTAAAGAAGAACTTCGCAATTGGAGCTTAAT 1211
Db 1198 GGTCGCGACCGCGGTGTCAGTCAGGCGCAAGACCGATCGGAGCTGGAGCTAGAC 1257
Qy 1212 GCTACACGGTGGAGCGGTGAGAAGAGTGTGCGTGTGAGCAGACTTTAGC 1271
Db 1258 AATGCCAAGGCGCGCTGGAGGCACTGGCGGGGGTGTGAGCCGTGCAA 1317
Qy 1272 GTRATGAAAGTAGCAGCTGTGAGCTGAGGGATGATCTACTGACATTCATT 1331
Db 1318 GCGCCCGACCCCTGAGGAGCTGAGCTGAGCTGAGCTGAGGAGGCGACACATC 1377
Qy 1332 GTGCTTCGCTCTAGAGAGGCTGTTACCTAAATGCTTTAAATGTTGGTAAAGAGC 1391
Db 1378 GTGAGGGGGCGAGGCCCGCTGAGCAGATGCGCTTAACTCGCGCTGAGACCG 1437
Qy 1392 TCGTACTGATGACAGTGTAAACACGCTTGGAGGACAGGATTATGTCRACA 1451
Db 1438 GGCGTGGTGGCGAGAGGGTGGCAGCTGGCGGCGCAACTGAGCTGACCGAC 1497
Qy 1452 GGTCAGGGGTGATGATGATTAACAGGACGATCTGACCCGCTCAAACTACAGTCA 1511
Db 1498 GGTCGCTACAGGAGTCCTGCGCCCGCTGTGACCCGCTGAGGTCAGCGT 1557
Qy 1512 GGCTCTAAATGAGCTCTGAGCTGAGCTGAGGAGCTGAGGAGCTGTTGGCT 1571
Db 1558 GGCTCGAGATGGGGTCATGGGGGTGTCTGACCAACCCGGGGCGTGTG 1617
Qy 1572 ATAAACCTGA 1583
Db 1618 GACAAGCGGAA 1629
```

```
; NAME/KEY: CDS
; LOCATION: (1)...(1944)
; US-10-267-311-28
```

```
Querry Match 27.7%; Score 460; DB 9; Length 1947;
Best Local Similarity 55.8%; Pred. No. 9. 9e-103; Mismatches 605; Indels 0; Gaps 0;
```

```
Qy 12 CATTGCAAAAGAACTCAATTTCACAGATGGCGATGGCGAGAGT 71
Db 322 CATTGCAAGACAACTGGTAGAGAGAGGCGCCCTCGGGCCTGAGGGGCTG 381
Qy 72 GATATTTAGCAGTACCGCAGAAGTACGCTGTTGTTCTAAAGGGCGCAATGTTCT 131
Db 382 AAGCCCTCCGCAAGGGTAAAGGTGACATGGGCAATGGGCAAGGGCGAACCTGGC 411
Qy 132 GAAAGCTTTGTTCTCTTAACTATRACATRACGGGTAACCATGCTAAAGAGTC 191
Db 442 GAAAGACTGGTGCCCCCAGTACCCAGATGGTGTCCATGCCAGGAGTC 501
Qy 192 GATTAAGAGTATTTGAAACATGGGCAAAATGGGCTGAGTGTGCTCTAA 251
Db 502 GAGCTGGAGATCCTGAGCAGAGAATGGGCCAGTTGGCAAAAGAGTGGCAGAG 561
Qy 252 ACCATGATATGCTGTTGAGGACACTACTCCACAACTGTTGACAAAGCATTG 311
Db 562 GAACTGAGCTGGCCCGTGCACGACGCCGCGCCGCGCGCGCGCGCGCGCG 621
Qy 312 CATTGAGGACTAAATGAGCAGAGCAGGGCTRACTCAATGGTATCGTGGAGCA 371
Db 622 CGGAGGCGCTGCGCACGCGGGGCCACCGCGCGCGCGCGCGCGCGCGCG 681
Qy 372 GAAAGACAGCACAGCACACSTGTTGAGCTGACCCATTGTCACCTGATCTGC 431
Db 682 GAAAGCCGCTGAGGAGGTACCGAGACACCTGCTCAAGGGCCAAGGGTGGAGAC 741
Qy 432 AAGGAGCTATGCTGAGCTGCTGAGTACCTCAGGCTCTGAAAGTTGGAGAT 491
Db 742 AAGGAGCAGATGGGCCACCGAGGATTGCGGGTGGACAGTCATGGTACCTG 801
Qy 492 ATCTAGAGCTATGAGGTTGGCGCAAGGAGTGTGTTGATACATGAGAAATCTCGA 551
Db 802 ATGCCGAGGCGATGAGCAGTGGCAACAGGGGCCATCACCGTGAGGACTCAC 861
Qy 552 GGTATGAAACAGAAGTGGTGTGAGGATGCAATTGACCTGGTACCTG 611
Db 862 ACCTTGGCGTCACGCTCGAGTCACCGAGGTTGGGTCACAGAGCTACATCG 921
Qy 612 CAATACAGGGTACAGACAGTGGTGTGAGGATGCAATTGACCTGGTACCTG 671
Db 922 GGTATGAGTGGTACGACGACCTGGCTGAGGAGCTGGCTGGAGGACCCCTACATCTG 981
Qy 672 ATCCGGTAAAGATGCAACACCCAGACATTTGCACTACTTGGAGGTCT 731
Db 982 CTGGTCAGCTCAGGGTGCACCTGCAAGGATCTGCTGCGCTGAGAGTCATC 1041
Qy 732 AAAACCAACCGCCCTTACTTATGAGTGTGGAGTGTGAGACTCCAC 791
Db 1042 GGACCGCTAAGCCCTGCTGAGCATGTCATCTGAGGTTGAGCTAC 1101
Qy 792 CTGCTCTGAAAGATGTTGGTACTTCATGTTGCTCTCAAAGGCGAGGTT 851
Db 1102 CTGGTCGTCACAAAGATCGCGGACACTTCAGTGGTGGCTGAGACTCCAC 1161
Qy 852 GGTATGCTGAAAGCTGAGCATGTCATCTGAGGTTGAGCTAC 911
Db 1162 GGCCACCCGCAAGCGATGCGCTGGAGGATGCGCTACCCGGTGGAGTC 1221
Qy 912 ACAGAGTGTGAGCTGAAAGATGCTACATGACCCCTTGACAGCTG 971
Db 1222 NGCGAAGGGCTGGCTACCGTGGAGAACCGCGACTCTGCTGCAAGGGCGTC 1281
Qy 972 AAGATTAGCTGATTAAGATAGCACAGACTTGTGAAAGGTCAGGAAGTCAGAGC 1031
```

```
RESULT9
US-10-267-311-28
; Sequence 28, Application US/10267311
; Publication No. US20030050479A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILING DATE: 2001-02-01
; CURRENT APPLICATION NUMBER: US/10-267-311
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1995-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FASTSBQ for Windows Version 4.0
; SEQ ID NO: 28
; LENGTH: 1947
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: fusion sequence
```


OTHER INFORMATION: fusion sequence
; FEATURE: -
; NAME/KEY: CDS
; LOCATION: (1)...(1620)
; US-10-267-311-3

Query Match 27.6% Score 458.6: DB: 9; Length 1623;
Best Local Similarity 55.8%; Pred No. 2e-102; Matches 875; Conservative 0; Mismatches 694; Indels 0; Gaps 0

QY 915 GAGGAGCTAGACTGTGATTAAGATGCTACATGACGCCCTGGACGGTGTGAG 974
Db 901 GAGGAGGTGGCTGAGGCTGAGGCTGGAGAAGGCCGACTTGTGCGCTAGGAAAGCCGCAAG 960

QY 975 ATTAAGTGTGATTAAGATGACAGTAACTGTTAGCTAGGAGTCAGAGCTT 1034
Db 961 GTCGGTGTGACCRAGGAGCACCATGTCAGGGCGCGGGAGACCGACGCATC 1020

QY 1035 GTCAGCGATGCTGAGTATAATGCAATTAGAACACAACTTCGACCTTGACCT 1094
Db 1021 GCGGGAGCTGAGTGGCCAGATTCGCCAGAGATCGAACAGCGACTCGACGCCT 1080

QY 1095 GAAAACTACAGAAGCTTGGGAATTAGCTGCTGTTGAGCTGATCAAGTASCA 1154
Db 1141 GCGCGCACCGAGTGAACATCAGGAGGCAAGGCCCATCGAGATGCGGTGCGAT 1200

QY 1155 GTCGCAACAGACACCTTTAAAGAATTAACCTGGATGAGACAGCGACTCGACGCCT 1214
Db 1201 GCGCAGGCGCGCGAGGAGGSCATGTCGCGGTGGGGTGCACCTGCAAGG 1260

QY 1275 ATTGAAAGAATGAGCTCTTGACTGAGCTTGAGGCGATGATGCTACTGGAGTACATTTG 1334
Db 1261 GCGCCGACCCCTGGAGGCGACGGCGACGCCAACCTGGCCACACTCTG 1320

QY 1335 CTTCGTGCTCAGAAGAGCTGTACGTCAAATGCTTTAATGTTGGTACAGGCGCC 1394
Db 1321 AAGGGGGCGCTGAGGCGCCGGTGAAGATGCCCTCACTCGGCGTCAAGCGGC 1380

QY 1395 GTACGTGATGACACTGAAACACCTGGAGGAGATTAATGTCGACAGCT 1454
Db 1381 GTGGGGCGCGAGAAGTGGCGCACCCGCGCGCGACCGACTGACGCTAACCGT 1440

QY 1455 GAGGGGGTGAATGATTAACAGAACTATGACCTCTGCAAGATGACATCGG 1514
Db 1441 GTCCTACGGAGCTCTCCCTGCCCGCGTGGACCCGCTCAG 1500

QY 1515 CTTCAAATGAGCTCTGAGCTATTTGACACAGAGCAGTGCTGAT 1574
Db 1501 CTGGAGAATGGGGCTCATGGGGCTGTCTGTGACCCGGCGCTGGCGAC 1560

QY 1575 AACACTGAA 1583
Db 1561 AACCGGAA 1569

RESULT 11
US-10-267-311-3

: Sequence 3, Application US/10267-311
; PUBLICATION NO. US20030050469A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/000201
; CURRENT APPLICATION NUMBER: US10/267,311
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIORITY FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1623
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

us-10-267-311-16

Query Match 27.6%; Score 458.6; DB 9; Length 1920;
Best Local Similarity 55.8%; Pred. No. 2.2e-02; Mismatches 694; Indels 0; Gaps 0;

Matches 875; Conservative 0; Mismatches 694; Indels 0; Gaps 0;

QY 975 ATTACAGTGTAAAGATGAGCACAACTAATGTCAGGTCAGAGTCATT 1034
Db 961 GTCGTTGTCACCAKAGGAGCACCCATGTCAGGCGCCGTCACCGACGCC 1020

QY 1035 GCTAACCTATGTCACATTAATGCAATGAGAACACACTCTGTCAGCT 1094
Db 1021 GCGGAGCAGGCGCAGTCAGGAGTCAGGAGTCAGGACACTCGCTGACCGT 1080

QY 1095 GAAAACTACAGAACGAGCTTGCGGAATTAAGTGGCTGAGCTTATCAAGTGG 1154
Db 1081 GAGAGCTGTCAGGAGCGCTGCGCAGCGCGGTCGCGTGCAGCAGGGT 1140

QY 1155 GTCACACAGAGACGCTTAAAGAAATGAACTTCGGATTGAGGTCAATGCT 1214
Db 1141 GCCGCCACCGAGTCAGCTACAGGAGCTGGATGGGATGGGTCCAA 1200

QY 1215 ACAGTGTGAGCGCTGAGGAGTATCTTGTGAGGGCAACGACTTACGGT 1274
Db 1201 GCGCAGGCGCGTCAGGAGGGCATGCGCAGGGCTGAGCGTCAATGCG 1260

QY 1275 ATTGAAAGAATGAGACGCTTGAGGAGTATCTTGTGAGGGCAACGACTTACGGT 1334
Db 1261 GCGCCGACCCCTGAGGAGCTGAGTCAGTGCAGGCGAGGAGCGCCACATGCG 1320

QY 1335 CTGGTGTGCTAGAGACCCCTGAGTCAGTGCAGGAGCTGAGGCTCC 1394
Db 1321 AAGGTGCGCTGAGGAGCCCTGAGTCAGGAGCTGAGGAGCTGAGGCTCC 1380

QY 1395 GACTTATGAGTCAGTGTGAAACAGCCCTGAGGAGCAGGTTATCTGACAGT 1454
Db 1381 GTGCTGGCCGAGAAGTGTGCGAACATGCGGCTGCGGCTGGCCAGGACTGACCGT 1440

QY 1455 GAGTGGTTGATGATTAACCGGAATCATGGCCCTGTCAGAGTCACCGATAGCG 1514
Db 1441 GTCTACAGGAGCTGCTGCGCCGCTGCTGAGGCTGG 1500

QY 1515 CTCCAAATGAGTCAGTGTGAGTCAGTGTAAATGAGACACGAGCAATTGCTAAT 1574
Db 1501 CTGCAAGATGCGGTCATGCGGGCTGCTGACCCACCGAGGCCGTCGTCAGCG 1560

QY 1575 AAGCTAA 1583
Db 1561 AAGCGGAA 1569

RESULT 12
US-10-267-311-16
; Sequence 15, Application US/10267311
; Publication No. US20030030469A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10-267,311
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 1920
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE: OTHER INFORMATION: fusion sequence
; FEATURE: NAME/KEY: CDS
; LOCATION: (1)...(1917)

QY 615 TACATGGCACAGACATTAACATGGTCAGACCTTGAAACCGATTATCTAATC 674
Db 601 TACCTCGGACCGCGCCGGAGGCTCAGGGCTGAGGCTGAGCCCTACATCTG 660

QY 675 ACGGATAAAAGTCACATCCAGAACATTGGCACTACTTGAGGAGTCCTAA 734
Db 661 GTCAGCTCAAGGTGTCACCTGCAAGGATCTGCGCTGCGTCAGGAGGTCATCGGA 720

QY 735 ACCACCGCTCATRACTCATTTGAGGATGCTGAGGCTGAGGACACTTCACCTT 794
Db 721 GCGGTAAGCGCTCTGATCATGCGGAGGAGCTGGCGAGGCGCTGTCACCGT 780

QY 795 GTCCTGACAAAGATGCTGTTGACTCTCAATGTTGCTGTCAGGCGCAGGATTGT 854
Db 781 GTCCTCACAGATGCCGCCGACCTCTGAGGCTGCGCTGAGGTCAGGCTGCTAG 840

QY 855 GATGGTGTAAAGTGTGAGGACATTGCTGAGGAGTCAGTGTGAGGAGTCACCTT 914
Db 841 GACCGCCGCAAGGGAGCTGCGAGATGTCAGCTTCACCGTGTAGGAGTCAGC 900

QY 915 GAGGATCTAGACTGTAAAGATGTTATGACGCTGAGGCTGAGGAGTCAGGCTG 974
Db 901 GAGAGGCTGACGCTGAGGACGCCGACCTGCTGCTGAGGCGCGCAAG 960

QY 975 ATTACAGTGTAAAGATGAGCACAACTAATGTCAGGTCAGGAGTCAGAGTCATT 1034
Db 961 GTCGTTGTCACCAAGGAGCACCCATGTCAGGCGCCGTCAGCAGGCCATC 1020

1583 ACCGTAGAGAGCTGGAGGAGCGCTGGCAAGGTGGGGGTGGTGGCGGTGATCAAGG 1642
 QY 1150 TAGGAGCTCAGACAGAGACGCTTAAAGARTGAACCTCCATGAGATCTCAA 1249
 Db 1643 CGCGGCGCCACCGAGGCGCAGACGAGCTCAAGAGGCCAGACCCGATCGAGTC 1702
 QY 1210 ATGGTACGCTGACCGCTGAGAGGATCTGGTGGGGTGGAGACGCAATTA 1269
 Db 1703 GCAATGCGCAAGGCCCTCGAGGGCATGTCGCCGCTGGGGTGGAGCTGTG 1762
 QY 1270 CGGTATGAGAAAGTAGCCTCTGAGCTAGGGGATCTGGGGTGGAGACGCA 1329
 Db 1763 AAGGGGCCGACCTGGAGCTGAGACGAGCTGAGCTGAGGAGCAACCA 1822
 QY 1330 TTGGCTCTCGCTCTAGAAGAGCTGAGCCTAAATGCTTAATGCGGGTACGAG 1389
 Db 1823 TCGTGAAGGGCTGGCGCTGGAGGCCCGCTGAAGCAGATCGCTCAACTCGGGT 1882
 QY 1390 GCTCGTGTAGTATGACAGTGTAAACAGGCCGAGAACAGATAATGCGCAA 1449
 Db 1883 CGGGCGGCTGAGAGGCGCAACCTCCGCTGGAGCTGAGCTGAGCTGAGA 1942
 QY 1450 CAGGTGAGTGGGTGATGAGTAAACGGAGATCATGACCTGTGAGCTGAGA 1509
 Db 1943 CGCGTGTACGAGATGTGCTGCGGCTGCTGACCGGGCTGTTCCGAC 2002
 QY 1510 CAGCGCTCAAAAGCAGCTCTGAGTAGCTTAAATGAGAACAGAGCTGGT 1569
 Db 2003 CGCGCTGAGAATGCGGTCATCGGGGCTGTTCCGACACCGGGCAAGTGC 2062
 QY 1570 CTATAAACGCGAA 1583
 Db 2063 CGGACAGCGGAA 2076

RESULT 15
 US-09-730-626-2986
 Sequence 2886, Application US-09738626
 Publication No. US20020197605A1
 GENERAL INFORMATION:
 APPLICANT: NAKAGAWA, SATOSHI
 APPLICANT: MIZOUSHI, HIROSHI
 APPLICANT: ANDO, SEIKA
 APPLICANT: HAYASHI, MIKRO
 APPLICANT: OCHINI, KEIKO
 APPLICANT: YOKOI, HARUHIKO
 APPLICANT: TATEISHI, NAOKO
 APPLICANT: SENOU, ANIHIKO
 APPLICANT: IKEDA, MASATO
 APPLICANT: OZAKI, AKIO
 TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 FILE REFERENCE: 249-125
 CURRENT APPLICATION NUMBER: US-09738, 626
 CURRENT FILING DATE: 2000-12-08
 PRIOR APPLICATION NUMBER: JP 99-377484
 PRIOR FILING DATE: 1999-12-16
 PRIOR APPLICATION NUMBER: JP 00-159162
 PRIOR FILING DATE: 2000-04-07
 PRIOR APPLICATION NUMBER: JP 00-280988
 PRIOR FILING DATE: 2000-08-03
 NUMBER OF SEQ ID NOS: 7059
 SOFTWARE: PatentIn ver. 3.0
 SEQ ID NO: 2986
 LENGTH: 164
 TYPE: DNA
 ORGANISM: Corynebacterium glutamicum
 US-09-730-626-2986

Db 1 ATGGCAAGATCATCCCTTGTAGAGAGCAGCTGGCTGAGAAAGGATGAC 60
 QY 75 ATGTTAGAGATACCGCTCAAGATGACCTGGTGTCTAAAGGGCAATGTTCTGAA 134
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 Db 121 AAGGCTTGGGGTGCCTCACCCACCATGAGCTGGTGCACATGAGCTGAG 180
 QY 195 TAGAGAGCATTTAAACATGGGCAAATGGTGTGAGGGCTGCTTAAAC 254
 Db 181 CTGAGATCTTACCGAGAGATGGGGCAGCTGGTCAAGGAGTC 240
 QY 255 ATGAGATATGCTGTTATGGAGGACTACTGCAACAACTTGTGAGCTGAG 314
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 Db 301 GAGGCTGCGCAACCTTGTGCTGCTAACCAATGSCACAGCCTGAG 360
 QY 375 ACACGACAGCACACGCTGTGAGCCCTGAAACCTTGTGCACTGTGAG 434
 Db 361 AGGTGTTGCTGAGTAATGAGACGCTGAGCTGAGCTGGAGGAGTGGAGC 420
 QY 435 GAAGCTTGTGTCAGGTGCTGAGCTGAGCTCATGCGCTGAGAAAGTTGGAGATATC 494
 Db 421 GAGCAGATGCTGCTTACCGCTGGTATCTCCGCACTGACCCAGGT 480
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 QY 540 GAGGATCTGGAGGTTGAGAACAGACTGAGTGAAGTGGTTGAGGAGCATGCTTGGCGT 599
 Db 541 GAGAGTCCAAACTTCTCGGTACTTCGTTGAGCTGCGAGGTTACTGAGCTGTTGAGAT 600
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 Db 601 GGCTCATCTCTCGGTACTTCGTTGAGCTGAGGCTCGAGGTTGCTGAGAT 660
 QY 660 CCATTAATCTTATCAGGATAAAAGGTCACACTCCAAAGACTTGTCCACACTT 719
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 QY 780 GCACCTCACCCCTGCTGACAAAGATGCGGTTACTCTCATGTTGAGCTCAA 839
 Db 781 GCTCTGTCACCCCTGCTGACAAAGATGCGGTTACTCTCATGTTGAGCTCAA 840
 QY 840 GGGCAGGATGGTGTGCTGAGCTATGCTGAGACATGCTATGTTGAGCT 899
 Db 841 GCTCGGGCTTGGGGCAGACTGCTGAGCTGAGACATGCTGTTGCTCCAGGT 900
 QY 900 GGTACAGTACAGGAGCATGCTGAGTAAAGATGCTACATGAGCTGAGCCCT 959
 Db 901 GGCCTGGTCATTCGAGAGGTGGCTCCTGAGACGCGTGTGATCTCCACTCTA 960
 QY 960 GGACGGGTGCTTAAATCACATGAGTAAAGATGAGCACTAATGTTGAGGTGAG 1019
 Db 961 GGCCTGGTCATTCGAGAGGTGGCTCCTGAGACGCGTGTGATCTCCACTCTA 1020

Db	QY	1081
Db	QY	TTCCGACTTCGACGCCGCTACAGCGCTTCGGCTAAGCTTSCCGCGGCGTTGCA 1140
Db	QY	1140 GTTATCAACAGGAGCTCAACAGACGCTTAAAGAATGAAACTCGATTTGAG 1199
Db	QY	1141 GTGCITTAAGGGGGCGCACTACCGGGTTGACTCAAGGGCGACGCCATGGAG 1200
QY	QY	1200 GATCTCTAAATGCAACAGCAGCCACCGCTGAGAAGCTTCTGGTGGGACA 1259
Db	QY	1201 GATGCTGTCGCTAACGCTTAAAGGCCGCTGAGGGCTTCCSCCGGCGTT 1260
QY	QY	1260 GCATTTAATGGTTATGAAAGAATAG--GAGGCTTGACGTTAGGGATGATGCT 1316
Db	QY	1261 GCGCTGTCGAGCTCTACGTTCTGGACAACGAACTTGAGCTTCCGGCGAGGAGCA 1320
QY	QY	1317 ACTGGAGCTAACTATTGCTCTGCTCTAGAGAGCCGCTGAGTAAATGTTAAAT 1376
Db	QY	1321 ACCGGCTTCCATGTCGCCGGGAGCTCTGACTCTGTCCTCTGAGGAGATCGGTCTAC 1380
QY	QY	1377 GCTGGTACGAGGCTCGTGTAGTTTACAGTGTAAAGAAAAAGCCCTSCAGGAAGAGGA 136
Db	QY	1381 GCTGGCTGAGGGTCTCTGCTGAGGTTCCAGCTCCACAGGGGGCC 1440
QY	QY	1437 TTAACTGCAACAGGAGGTTGATGATGATTAACAGGAACTTGGCTGCTTC 1496
Db	QY	1441 CTCAACCTGCAACAGGCCGACTAGTCGACCTCAGGGCGGCACTACAGGCGGAGT 1500
QY	QY	1497 AATGAACTACGATTAAGCCTCAAAATGCACTGTTGAGCTGTTTATGACACA 1556
Db	QY	1501 AATGTCACCGCTCGCACTTCAGAACCTGCTGATCATGCGCTGCTGCTTC 1560
QY	QY	1557 GAAGCAGTGTGCTTAATAACCTGAAACCGAGCTAGGCCAG 1597
Db	QY	1561 GAGGCTGTCGCTGCTGACAAGCCACACCTGCGAGCGGAGC 1601

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